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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

Title: Perfect score: US-09-331-631A-3_COPY_117_185 384

Sequence:

1 NRQRDPQQQYEQCQERCQRH.....EEQQREDEEKYEERMKEEDN 69

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 88757 segs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

85.5	86 22.	86.5 22.	87 22.	87.5 22.	88 22.	89.5 23.	90 23.	90.5 23.	90.5 23.	90.5 23.	90.5 23.	90.5 23.	91 23.	92 24.	92.5 24.	93 24.	94 24.	94 24.	94 24.	94.5 24.	94.5 24.	94.5 24.	95.5 24.	96 25.	96 25.	97 25.	98 25.	98 25.	110 28.	113 29.	133 34.	49.5 38.	No. Score Match	Result Query	•
3 47 1	386	2038	1023	708	1.240	743	338	1905	1048	695	573	550	905	1157	758	1403	1549	1085	5 1023	9	877	678	538	524	429	2124	648	482	1407	4 1898	6	9	ch Length DB	Ÿ	
AGRP_LUFCY	ARP4_STRPY	FSH_DROME	CLOC_DROME	GBF_DICDI	YNJ1_YEAST	ABRA_PLAFC	LEGB_PEA	TAGB_DICDI	SRA4_RAT	XE7_HUMAN	GLB1_MATZE	BLSA_HUMAN	SNF5_YEAST	Y182_HUMAN	YM38_YEAST	PRO_DROME	TRHY_SHEEP	YAFA_SCHPO	GLT_DROME	SIMA_DROME	CHIC	GARP_PLAFF	_	SBP_SOYBN	1	•	KAPC_DICDI	ŀ	ı		Σ	VCLB_GOSHI	ID		
	P13050 streptococc	d	drosophila	dictyostel	P53935 saccharomyc	plasmodiu	pisum sati	dictyo	ratt	homo	zea			5		drosc	O		P33438 drosophila	drosophila	P53352 gallus gall		saccharomy	qlycine	macaca fas	93074 homo	34099 dictyostel	15696 homo	7709 oryc	7283 homo sapie	9799 gossypium	P09801 gossyp	Description		

Dр Qy DЬ QΥ

1 NRORDPQQQYEQCQERCQRHETEPRHMQTCQQRCERRYEKEKRKQQKRYEBQQ------- 53
:| |||::||:||: || || ||||| :||:|::| |
78 HRPEDPQRRYEECQQECR--QQEERQRPQCQQRCLKRPEQEQQQSQRQFQEQEQQHCHQQE 135

85.5 22.3 471 RU17_XENLA 85.5 22.3 471 RU17_XENLA 85.5 22.3 572 I MOGS_LYTVA 85 22.1 285 I INVO_CANFA 85 22.1 285 I INVO_CANFA 85 22.1 1178 I MNN4_YEAST 85 22.1 1344 I IF3A_MOUSE 85 22.1 1342 I IF3A_PLAFF 84 21.9 479 I UZR1_HUMAN 81.5 22.0 321 I ABRA_PLAFF 84 21.9 479 I UZR1_HUMAN 83.5 21.7 347 I INVO_PIG 83.5 21.7 444 I CEB_DROME 83.5 21.7 605 I GLCA_SOYBN 83 21.6 389 I M49_STRPY	22.3 572 22.3 572 22.1 285 22.1 1344 22.1 1382 22.1 1382 22.1 1382 22.1 382 21.7 347 21.7 347 21.7 605 21.7 605 21.6 389	45	44	43	42	41	40	39 .	38	37	36	35	34
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ALIGNMENTS

M B Ou	DR DR DR DR FT FT	888888888	CCCCCCRPTTT	RESULT VCLB_G ID VCLB_G ID V ID
Ouery Match 38.9%; Score 149.5; DB 1; Length 588; Best Local Similarity 33.7%; Pred. No. 1.3e-05; Matches 30; Conservative 21; Mismatches 15; Indels 23; Gaps 3;	EMBL; M16891; ANA33071.1; PIR; A30838; FWCKAB. HSSP; P50477; 1CAX. INTERPRO; IPRO01113; PFAM; PF00546; SeedStore_7s; 1. Seed storage protein; Signal. SIGNAL 1 25 CHAIN 26 588 AA; 69729 MW; 63E699B29AB8ADEB CRC64;	SWISS-PROT entry is copyright. It is produced the een the Swiss Institute of Bioinformatics and t European Bioinformatics Institute. There are not by non-profit institutions as long as its confied and this statement is not removed. Usage by the requires a license agreement (See http://www.end.an.email.tollicense@isb-sib.ch).	is and the members of VACUOLAR PROTEIN ASECLIN, VICILIN,	ULT 1 B_GOSHI STANDARD; PRT; 588 AA. PO9801; 01-MAR-1989 (Rel. 10, Created) 01-MAR-1989 (Rel. 10, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) VICILIN C72 PRECURSOR (ALPHA-GLOBULIN B). Gossypium hirsutum (Upland cotton). Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

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VCLA_GOSHI
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Best Local
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Q07283;
Q1-OCT-1994
Q1-OCT-1994
                                                                                                                                                                                   HUMAN
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Gossypium hirsutum (Upland cotton).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
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01-MAR-1989 (Rel. 10, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
VICILIN GC72-A PRECURSOR (ALPHA-GLOBULIN A).
MEDLINE=93280194;
                                        Mammalia;
                                                       Eukaryota;
                                                                    Homo sapiens (Human).
                                                                                               TRICHOHYALIN
                                                                                                               01-OCT-2000
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P09799;
              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERPRO;
                                                                                                                                                                                                                                                                                               114
                                                                                                                                                                                                                                           174
                                                                                                                                                                                                                                                                     58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             titles requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                  OR TRHY OR THL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               storage protein;
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25; Conser
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Eutheria;
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 PubMed=7685034
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                                        Chordata;
Primates;
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                                                                                                            Last sequence update)
Last annotation updat
                                                                                                                                         Created)
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Pred. No. 0.00028;
8; Mismatches 23;
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; C9DB9371C976953B CRC64;
                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                           197
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                                                                                                                                                                                                                                                                                                                                                     Gaps
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"The structure of human trichohyalin. Potential multiple roles as a functional EF-hand-like calcium-binding protein, a cornified cell envelope precursor, and an intermediate filament-associated (cross-linking) protein.";

J. Biol. Chem. 268:12164-12176(1993).
                                                                                                                          CA_BIND
                REPEAT
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REPEAT
                                                                                                                                                                                                                                                         PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIFFERENTIATION.

- i SUBUNIT: MONOMER (PROBABLE).

- i TISSUE SPECIFICITY: FOUND IN THE HARD KERATINIZING TISSUES SITHE INNER ROOT SHEAT (IRS) OF HAIR FOLLICLES AND MEDULLA, AND THE FILIFORM PAPILLAE OF DORSAL TONGUE EPITHELIUM (PROBABLE)

- i - DEVELOPMENTAL STAGE: EXPRESSED DURING LATE DIFFERENTIATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epidermis."
J. Invest. |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O'Keefe E.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1731-1898
MEDLINE=93315897; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lee S.-C., Kim I.-G., Marekov L.N., O'Keefe Steinert P.M.;
                                                                                                        DOMAIN
                                                                                                                                                               DOMAIN
                                                                                                                                                                                Repeat;
                                                                                                                                                                                                   PROSITE; PS00018; EF_HAND; 1
PROSITE; PS00303; S100_CABP;
                                                                                                                                                                                                                                      PFAM;
                                                                                                                                                                                                                                                                                                             MIM; 190370;
                                                                                                                                                                                                                                                                                                                                                               EMBL; L09190; AAA65582.1;
                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Trichohyalin: a structural protein of hair,
                                                                                                                                                                                                                                                                          INTERPRO; IPRO02048;
                                                                                                                                                                                                                                                                                        INTERPRO: IPR001751;
                                                                                                                                                                                                                                                                                                                            HSSP; P02633; 1BOC.
                                                                                                                                                                                                                                                                                                                                            PIR; A45973; A45973.
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4; PF00036; efhand; 1.
ITE; PS00018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: CONSISTS OF NINE DOMAINS. DOMAIN 1 CONTAINS TWO EF-HAND CALCIUM-BINDING DOMAINS. DOMAINS 2-4, 6, AND 8 ARE ALMOST ENTIRELY ALPHA-HELICAL, CONFIGURED AS A SERIES OF PEPTIDE REPEATS OF VARYING REGULARITY, AND ARE THOUGHT TO FORM A SINCLE-STRANDED ALPHA-HELICAL ROD STABILIZED BY IONIC INTERACTIONS. DOMAIN 6 IS THE MOST REGULAR AND MAY BIND KIF DIRECTLY BY IONIC INTERACTIONS. DOMAIN 5 AND 7 ARE LESS WELL ORGANIZED AND MAY INDUCE FOLDS IN THE MOLECULE. DOMAIN 9 CONTAINS THE C-TERMINUS, CONSERVED AMONG THE MOLECULE. DOMAIN 9 CONTAINS THE C-TERMINUS, CONSERVED AMONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: INTERMEDIATE FILAMENT-ASSOCIATED PROTEIN THAT ASSOCIATES IN REGULAR ARRAYS WITH KERATIN INTERMEDIATE FILAMENTS (KIF) OF THE INNER ROOT SHEATH CELLS OF THE HAIR FOLLICLE AND THE GRANULAR LAYER OF THE EPIDERMIS. IT LATER BECOMES CROSS-LINKED TO KIF BY ISODIPEPTIDE BONDS. IT MAY SERVE AS SCAFFOLD PROTEIN, TOGETHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: KNOWN SUBSTRATE OF TRANSGLUTAMINASE. SOME 200 ARGININES ARI PROBABLY CONVERTED TO CITRULLINES BY PEPTIDYLARGININE DEIMIDASE SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE S-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WITH INVOLUCRIN, IN THE ORGANIZATION OF THE CELL ENVELOPE OR EVEN ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN ITS OWN CALCIUM-DEPENDENT POSTSYNTHETIC PROCESSING DURING TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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                                                                                                                                                                             Calcium-binding.
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 326
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                                                  SITE I (LOW AFFINITY) (POTENTIAL)
SITE II (HIGH AFFINITY) (POTENTIA
6 XI 3 AA TANDEM REPEATS OF
R-R-E-Q-E-E-E-R-R-E-Q-Q-L.
1-1 (APPROXIMATE).
1-2 (APPROXIMATE).
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 1-3
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Matches 25
                                                                                                                                                                                                                  Fietz M.J., Rogers G.E.;

Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: INTERMEDIATE FILAMENT-ASSOCIATED PROTEIN THAT ASSOCIATES IN REGULAR ARRAYS WITH KERATIN INTERMEDIATE FILAMENTS (KIF) OF THE INNER ROOT SHEATH CELLS OF THE HAIR FOLLICLE AND THE GRANULAR LAYER OF THE EPIDERMIS. IT LATER BECOMES CROSS-LINKED TO KIF BY ISODIPETPIDE BONDS. IT MAY SERVE AS SCAFFOLD PROTEIN, TOGETHER WITH INVOLUCRIN, IN THE ORGANIZATION OF THE CELL ENVELOPE OR EVEN ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK.
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Eukaryota; Metazoa; Chordata; (
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01-OCT-1994
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                                                                SUBUNIT: HOMODIMER (PROBABLE).
TISSUE SPECIFICITY: FOUND IN THE HARD KERATINIZING TISSUES S
THE INNER ROOT SHEAT (IRS) OF HAIR FOLLICLES AND MEDUILA, AN
THE FILIFORM PAPILLAE OF DORSAL TONGUE EPITHELIUM (PROBABLE)
DEVELOPMENTAL STAGE: EXPRESSED DURING LATE DIFFERENTIATION THE EPIDERMIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA TANDEM REPEATS OF R-R-E-Q-Q-L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A A
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                                                                                                AND
                                QF
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U2R2_HUMAN

D U2R2_HUMAN

AC Q15696;

AC Q15696;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE U2 SMALL NUCLEAR RIBONUCLEOPROTEIN AUXILIARY FACTOR
                                                                                                                                                                                                                                                                                                     RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA_BIND
SEQUENCE
                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restues by non-profit institutions as long as its content
                 Mukai T
                            Kitagawa K., Wang X.
Inazawa J., Abe T.,
                                                         MEDLINE=96163878;
                                                                            TISSUE=BRAIN;
                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                U2AF1-RS2 OR U2AF1RS2.
                                                                                                                                                                                 RELATED-PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERPRO; IPR002048; -. PFAM; PF01023; S_100; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00036; efhand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <del>.</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat; Calcium-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERPRO; IPR001751;
 Isolation and mapping of human homologues of an
                                                                                                                                                                                                                                                                                                                                                  314
                                                                                                                                                                                                                                                                                                                                                                                                         256 QQQLRRELEEIREREQRLEQEERREQ -- QLRREQRLEQEERREQQLRRELEEIREREQRL 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN: CONSISTS OF NINE DOMAINS. DOMAIN 1 CONTAINS TWO EF-HAND CALCTUM-BINDING DOWAINS. DOMAINS 2-4, 6, AND 8 ARE ALMOST ENTIRELY ALPHIA-HELICAL, CONFIGURED AS A SERIES OF PEPTIDE REPEATS OF VARYING REGULARITY, AND ARE THOUGHT TO FORM A SINGLE-STRANDED ALPHA-HELICAL ROD STABILIZED BY IONIC INTERACTIONS. DOMAIN 6 IS THE MOST REGULAR AND MAY BIND KIF DIRECTLY BY IONIC INTERACTIONS. DOMAINS 5 AND 7 ARE LESS WELL ORGANIZED AND MAY INDUCE FOLDS IN THE MOLECULE. DOMAIN 9 CONTAINS THE C-TERMINUS, CONSERVED AMONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: KNOWN SUBSTRATE OF TRANSGLUTAMINASE. SOME 200 ARGININES ARE PROBABLY CONVERTED TO CITRULLINES BY PEPTIDYLARGININE DEIMIDASE. SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE S-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAMILY.
SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING
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27; Conserv
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                            ; PubMed=8586425;
g X., Hatada I., Y
T., Mitsuya K., Os
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91
33
73
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SITE I (LOW AFFINITY) (POTENTIAL).

SITE II (HIGH AFFINITY) (POTENTIAL).

MW; AE17D2A159F12B7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 110; DB 1
Pred. No. 0.04;
19; Mismatches
                               Oshimura
                                              Yamaoka
                             X ⊢3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                             Nojima
Murata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
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imprinted mouse gene
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                            H.,
                                                                                                                                                                                            35 KDA SUBUNIT
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                               Monden
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Best Local
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P34099;
01-FEB-1994
01-FEB-1994
30-MAY-2000
MEDLINE=93066311; PubMed=1332055; Mann S.K.O., Yonemoto W.M., Taylor S.S., Firtel R.A.; Mann S.K.O., Yonemoto W.M., Taylor S.S., Firtel R.A.; PDdPR3, which plays essential roles during Dictyostelium development, encodes the catalytic subunit of cAMP-dependent protein kinase."; Proc. Natl. Acad. Sci. U.S.A. 89:10701-10705(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                   STRAIN-AX3
                                                                                CHARACTERIZATION
                                                                                                         Biochemistry
                                                                                                                   Anjard C., Etchebehere L., Pinaud "An unusual catalytic subunit for of Dictyostelium discoideum.";
                                                                                                                                                          MEDLINE=93385090;
                                                                                                                                                                         CHARACTERIZATION.
                                                                                                                                                                                                Buerki E., Anjard C., Scholder J.-C., Reymond C.D. "Isolation of two genes encoding putative protein during Dictyostelium discoideum development."; gene 102:57-65(1991).
                                                                                                                                                                                                                                                   MEDLINE=91323730;
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         Eukaryota; Dictyosteliida; Dictyostelium
                                                                                                                                                                                                                                                                                                    PKAC OR PK2 OR PK3.
Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                CAMP-DEPENDENT PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50102; RRM; 1.

Nuclear protein; Ribonucleoprotein
DOMAIN 46 49 POLY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00076; rrm; 1.
PFAM; PF00642; zf-CCCH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               125
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SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIE (RRM).
SIMILARITY: TO MAMMALIAN SPLICING FACTOR UZAF 35 KDA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             KROEK 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QRDPQQQYEQCQERCQRHETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERERQRLHEEWLLREQKAQEEFRIKKEKEEAAKKRQEEQERKLKEQWEEQQRKEREEEEEQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR000571;
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482 AA;
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4 (Rel.
) (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                         32:9532-9538(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                           28,
39,
                                                                                                                                                          PubMed=8373760;
                                                                                                                                                                                                                                                   PubMed=1864510;
                                                                                                                                                                                                                                                                                                                                                                     28, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 POLY-GLU.
58044 MW; 1DACC8A6CA4727A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.5%;
29.2%;
                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
N KINASE CATALYTIC SUBUN
                                                                                                                                                                                                                                                                                                       (Slime mold)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 98; DB
Pred. No. 0.15
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-GLU
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                                                                                                                                 s.,
the
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                                                                                                                                 Veron M., Reymond C.D.;
cAMP-dependent protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1
0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         There are no restrictions ong as its content is in
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Y192_HUMAN
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Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphorylation.
DOMAIN 58
DOMAIN 136
DOMAIN 233
DOMAIN 336
NP_BIND 342
BINDING 365
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MOD_RES
                                                                                                                                                                                               01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
                                                                                                                                                                                                                                                                    Y192_HUMAN
Q93074;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                       TISSUE=BONE MARROW
                                           SEQUENCE FROM N.A
                                                                                       Mammalia;
                                                                                                              Eukaryota; Metazoa;
                                                                                                                                   HOMO
                                                                                                                                                          KIAA0192
                                                                                                                                                                               HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00069; pkinase; 1. PFAM; PF00433; pkinase_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERPRO; IPRO00961; ...
INTERPRO; IPRO02290; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DICTYDB; DD02030; PKAC. INTERPRO; IPR000719; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M38703; -;
MEDLINE=96281124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144
                                                                                                                                                                                                                                                                                                                                                                                                   204 0000000000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; JQ1150; ;
P; P05132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAMP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A MAXIMUM AT CULMINATION.
                                                                                                                                 sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                               DEEKYEERMKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RQRDPQQQYEQCQERCQRHETEPRHMQTCQQRCERRYEKEKRK-----QQKRYEEQQRE 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS50011;
                                                                                       Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                        (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
PROTEIN KIAA0192 (FRAGMENT).
                                                                                                                                   (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Serine/threonine-protein kinase; ATP-binding; cAMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JQ1150.
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07; PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                   215
PubMed=8724849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
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PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223
223
250
590
350
365
459
                                                                                       Primates;
                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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THR-RICH.
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); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASN-RICH.
                                                                                       Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D0F9B3A48C58D084 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98; DB 1;
No. 0.19;
                                                                                                                                                                                                                                                                                           2124 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                       Hominidae;
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                        Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV).
                                                                                                                                                                                                                                                                                                                                                                                                              APA4_MACFA P33621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
                                                                                 Osada J., Pocovi M., Nicolosi R.J., Schaefer E.J., Ordovas J.M.;
"Nucleotide sequences of the Macaca fascicularis apolipoprotein C
and A-IV genes.";
Biochim. Biophys. Acta 1172:335-339(1993).
-i- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION
CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
LIPASE BY APOC-II, POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJ
COMPONENT OF HDL AND CHYLOMICRONS.
-i- SUBCELLULAR LOCATION: EXTRACELLULAR.
                                                                                                                                                                                                                     MEDLINE=93192330;
                                                                                                                                                                                                                                                                                                                                         APOA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2061 ООНООООООО 2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.; "Prediction of the coding sequences of unidentified human The coding sequences of 40 new genes (KIAA0161-KIAA0200) analysis of cDNA clones from human cell line KG-1."; DNA Res. 3:17-24(1996).
                                                                                                                                                                                                                                                                               Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                      Macaca fascicularis (Crab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
                                                                                                                                                                                                                                                  EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 21.4 tes 15; Conservative
            TISSUE SPECIFICITY: SECRETED IN PLASMA.

DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REDEATS (EACH
22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-
MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RQRDPQQQYEQCQERCQRHETEPRHMQTCQQ-----RCERRYEKEKRKQQKRYEEQQREDE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through
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                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
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                                                                                                                                                                                                                    PubMed=8448212;
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LIPID-BINDING DOMAINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 97; DB
Pred. No. 0.63
95; Mismatches
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POLY-GLN.
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POLY-GLY
GLN-RICH.
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                                                                                                                                                                                  Schaefer E.J., Ordovas J.M.; fascicularis apolipoprotein C-III
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LECITHIN: CHOLESTEROI
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SBP_SOYBN
ID SBP_SOYBN
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Best Local :
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                                                                                                                                                                                                                                                                                        Glycine max (Soybean).

Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
REPEAT
REPEAT
                                                                                                   Grimes H.D., Overvoorde P.J., Ripp K., Franceschi "A 63-kD sucrose binding protein is expressed and tissues actively engaged in sucrose transport."; Plant Cell 4:1561-1574(1992).
                                                                                                                                                                                                                                                                       Magnoliophyta; eudicotyledons; core eudicots; Fabales; Fabaceae; Papilionoideae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
DOMAIN
               -i- FUNCTION: PLAYS A ROLE IN SUCROSE TRANSPORT.
-i- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
-i- TISSUE SPECIFICITY: ASSOCIATED WITH THE PLASMA MEMBRANE
SEVERAL CELL TYPES ENGAGED IN SUCROSE TRANSPORT, INCLUDI
                                                                                                                                                                                     MEDLINE=93104680;
                                                                                                                                                                                                           TISSUE=EMBRYO;
                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 30-50.
                                                                                                                                                                                                                                                                                                                                                                                     SUCROSE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1994 (Rel. 01-JUN-1994 (Rel.
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nes 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; s29565;
; s30195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration -
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; s30195.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Robinson L.C., Hubbard E.J.A., Graves P.R., de Paoli-Roach A Roach P.J., Kung C., Haas D.W., Hagedorn C.H., Goebl M., Culbertson M.R., Carlson M.;

"Yeast casein kinase I homologues: an essential gene pair.";

Proc. Natl. Acad. Sci. U.S.A. 89:28-32(1992).
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                                      STRAIN=S288C / AB972;
MEDLINE=94378003; PubMed=8091229;
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1. Biol. Cell 3:275-286(1992)
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DEVELOPMENTAL STAGE: IN THE COTYLEDON, EXPRESSION IS NOT DETECTED UNTIL 10 DAYS AFTER FERTILIZATION. BETWEEN 10-19 DAYS AFTER FERTILIZATION. BETWEEN 10-19 DAYS AFTER FERTILIZATION, NO DAYS AFTER FERTILIZATION, NO
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PIR; S29521;
PIR; S48979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Iraqui I., Vissers S., Cartiaux M., Urrestarazu A.; "Characterisation of Saccharomyces cerevisiae ARO8 and encoding aromatic aminotransferases I and II reveals a aminotransferase subfamily."; Mol. Gen. Genet. 257:238-248(1998).

-!- FUNCTION: CASEIN KIMASES ARE OPERATIONALLY DEFINED PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan F., Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R., Vignati D., Wilson R.,
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INTERPRO; IPR002290; -.
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                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00069; pkinase; 1. PROSITE; PS00107; PROTEIN_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98151783; PubMed=9491083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-SIGMA 1278B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaudin M.;
                                                                                                                                                                                                                           LIPID
                                                                                                                                                                                                                                                                                       NP_BIND
                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                   Multigene
                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-38 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
463
                                                           403
                             55
                                                                                       N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AS SUBSTRATES.
AS SUBSTRATES.
SUBCELLULAR LOCATION: PLASMA-MEMBRANE BOUND.
SUBCELLULAR LOCATION: PLASMA-MEMBRANE BOUND.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
CASEIN KINASE I SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ween the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no re
QEQQLQQQQQQQQQ 475
                                                           QQQQQQQYAQKTEADMRNSQYKPKLDPTSYEAYQHQTQQKYLQEQQKRQQQQKLQEQQL 462
                             EDEEKYEERMKEE
                                                                                       RQRDPQQQYEQCQERCQRH-----ETEPRHMQTCQQRCERRY--EKEKRKQQKRYEEQQR
                                                                                                                     l Similarity
19; Conser
                                                                                                                                                                                                                                                                                                                            PS00107; PROTEIN KINASE ATP: 1.
PS00108; PROTEIN_KINASE_ST: 1.
PS50011; PROTEIN_KINASE_DOM; 1.
PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                             family;
69
75
98
188
188
537
538
367
538 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S29521.
S48979.
                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     profit
                                                                                                                                                                                               AA;
                                                                                                                                                                                          y; Membrane; Prenylation; Lipoprotein.

353
ATP (BY SIMILARITY).
83
ATP (BY SIMILARITY).
98
ATP (BY SIMILARITY).
188
BY SIMILARITY
188
BY SIMILARITY
6ERANYL-GERANYL (POTENTIAL).
538
GERANYL-GERANYL (POTENTIAL).
5367
K -> E (IN REF. 2).
AA; 61715 MW; 77344717818C2D17 CRC64;
                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 institutions as long as its content
                                                                                                                                  24.9%;
                                                                                                                     26;
                                                                                                                                  Score 95.5; DB Pred. No. 0.26;
                                                                                                                     Mismatches
                                                                                                                     21;
                                                                                                                                                 Length
                                                                                                                     Indels
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S CASEINS
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                                                                                                                  7;
                                                                                                                  Gaps
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INCE_CHICK
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GARP_PLAFF
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1990
01-JAN-1990
15-JUL-1999
                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
INNER CENTROMERE PROTEIN (INCENP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
         SEQUENCE FROM N.A.
MEDLINE=94012983; PubMed=8408220;
MACKAY A.M., Eckley D.M., Chue C.,
MACKAY A.M., Eckley D.M., INCENPS
                                                                                       Gallus gallus (Chicken)
Eukaryota; Metazoa; Cho
                                                                                                                                                        INCE_CHICK P53352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-89040048; PubMed-2903445;
Triglia T., Stahl H.-D., Crewther
                                                                             Archosauria;
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A54514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J03998; AAA29605.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid-rich protein (GARP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structure of a Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kemp D.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLUTAMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P13816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GARP_PLAFF
                                                                                                                                                                                                                          599
                                                                                                                                                                                                                                                                   546
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                                                                                                                                                                                                                                                                                       1 NRQRDPQQQYEQCQERCQRHETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKY 60
                                                                                                                                                                                                                        EEEEEEED 606
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                                                                                                                                                                                                                                                                   DKEEDKKEESKEVQE-----
                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACID-RICH
                                                                                      Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alveolata;
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120
372
417
576
605
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(Rel. 13, Last sequence up
(Rel. 38, Last annotation
ID-RICH PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A54514
                                                                                                                                                                                                                                             68
                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antigen;
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678
164
416
441
604
653
                                                                            Neognathae;
          D.M., Chue C., of the INCENPS
                                                                                      Chordata;
                                                                                                                                                                                                                                                                                                                                                                     80551 MW;
required
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26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crewther P.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal.
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                                                                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                        GLUTAMIC ACID-RICH PROTEIN.

15 X 3 AA TANDEM REPEATS OF K-K-X.

9 X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                       POLY-GLU.
7 X APPROXIMATE
for
                                                                            Craniata; Ver; Galliformes;
                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                               X APPROXIMATE X APPROXIMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FC27
                                                                                                                                                                                                                                                                                                                                                                    2A8F85606496EA9E CRC64;
                                                                                                                                                                                                                                                                                                              Mismatches
s (inner centromere proteins):
   association with microtubules
                                                                                                                                                                                                                                                                                                                       94.5;
No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemosporida;
                     Earnshaw W.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                  877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Papua New Guinea).
emosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                      Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Silva A.,
                                                                                                                                                                  ΑA
                                                                                                                                                                                                                                                                                                                        DB
.37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            that
                                                                            Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                              TANDEM
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                                                                                                                                                                                                                                                                                                                                                                                          REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                REPEATS.
                                                                                                                                                                                                                                                                                                                                    678;
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                                                                           Phasianinae;
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RESULT 13
SIMA_DROME
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                    Q24167;
15-DEC-1998
15-DEC-1998
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
VARIANT
VARIANT
                                                     SEQUENCE rkum w.m.
MEDLINE=96269411; PubMed=8682312;
Nambu J.R., Chen W., Hu S., Crews S.T.;
"The Drosophila melanogaster similar bHLH-PAS gene enc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities
or send a
                            single-minded.";
Gene 172:249-254(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell
Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                during interphase and with the centra J. Cell Biol. 123:373-385(1993).
-!- FUNCTION: MAY ACT AS CYTOSKELETAL
                                                                                                                                                             Eukaryota;
Pterygota;
                                                                                                                                                                                                           SIMA.
                                                                                                                                                                                                                        SIMILAR PROTEIN.
                                                                                                                                                                                                                                                                                            SIMA_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - -
                                                                                                                                                                                           Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                            Ephydroidea; Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                            606
                                                                                                                                                                                                                                                                                                                                                                    666 QERKKEQE 673
                                                                                                                                                                                                                                                                                                                                                                                               61
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SUBUNIT: HOMODIMER OR HETERODIMER (PROBABLE).

SUBCELLULAR LOCATION: NUCLEAR. IS RESTRICTED TO THE NUCLEUS IN SUBCELLULAR LOCATION: NUCLEAR. IS RESTRICTED TO THE CHROMOSOMES UNTIL EARLY INTERPHASE, REMAINS TIGHTLY BOUND TO THE CHROMOSOMES UNTIL EARLY METAPHASE, AND DURING LATE METAPHASE GETS CONCENTRATED IN LINEAR ARRAYS THAT TRANSECT THE METAPHASE PLATE BETWEEN THE CHROMOSOMES. AS ANAPHASE BEGINS TO MOVE TO THE SPINDLE MIDZONE WHERE IT IS INTIMATELY ASSOCIATED WITH THE BUNDLED MICROTUBULES. LATER IN ANAPHASE GETS CLOSELY ASSOCIATED WITH THE CELL CORTEX, AND BY TELOPHASE IS CONCENTRATED AT EACH SIDE OF THE MIDBODY IN THE INTERCELLULAR BRIDGE, WITH WHICH IT IS DISCARDED AFTER.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; INCENP I AND INCENP II (SHOWN
                FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAPABLE OF ALTERING THE MORPHOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                            RRRQDEEARKQKALQQEEEERRHKELMQKKKEEEQGERARKIAEQRQAEQEREKQLAAERE 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  division; Microtubules;
                                                                                                                                                                                                                                                                                                                                                                                               EERMKEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDPQQQYEQCQERCQRHETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDE---EKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z25419; CAA80906.1;
Z25420; CAA80907.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                            melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                 (Rel.
(Rel.
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716
257
471
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   EFFICIENT
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                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                37, Created)
37, Last sequence up
40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.6%;
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 DNA-BINDING
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Σ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 94.5; D
Pred. No. 0.47
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coiled coil; Centromere;
Alternative splicing.
COILED COIL (POTENTIAL).
MISSING (IN ISOFORM INCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E -> Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A -> T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFA703149F555352 CRC64
TRANSCRIPTIONAL ACTIVATOR.
REQUIRES DIMERIZATION WITH ANOTHER
                                                                                                                                                                                                                                                                                           1505
                                                                                                                                                                                                                                                 update)
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.47;
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ISOFORM INCENP
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                                                                                                                                                             Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELLULAR MICROTUBULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THAT
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                                                                       encodes
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                                                         Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 877;
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                                                                       protein
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RESULT 14
GLT_DROME
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Best Local
                                                                                                                                                                                  Matches
GLT_DROME STAN
P33438;
Q1-FEB-1994 (Rel. 2
Q1-FEB-1994 (Rel. 2
30-MAY-2000 (Rel. 3
GLUTACTIN PRECURSOR
GLT.
                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERPRO; IPR001610; -.
INTERPRO; IPR003015; -.
PFAM; PF00785; PAC; 1.
PFAM; PF00989; PAS; 2.
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SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN THE EMBRYO.
SIMILARITY: BELONGS TO THE BASIC HELIX LOOP-HELIX (BHLH) FAMILY
TRANSCRIPTION FACTORS. HIGHEST TO HIF-1 ALPHA.
SIMILARITY: CONTAINS 1 PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ween the Swiss Institute of Bioinformatics and the E
European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription regulation;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
           SPAC29E6.10C.
Schizosaccharomyces pombe
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INTERPRO; IPRO02018; -.
PFAM; PF00135; COESterase; 2.
PFAM; PS00941; CARBOXYLESTERASE_B_2; 1.
CARBOXYLESTERASE_B_2; 1.
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Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Glutactin, a novel Drosophila basement membrane-related glycoprotein with sequence similarity to serine esterases.";
EMBO J. 9:1219-1227(1990).
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9 KDA PROTEIN C29E6.10C IN C
Ascomycota; Schizosaccharomycetales;
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            (Fission yeast)
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WITH TYPE-B CARBOXYLESTERASE/LIPASES
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SEQUENCE 1085 AA; 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones L., Murphy L., McNeil A., Simpson I., Harris D., Barrell B.G., Rajandream M.A., Walsh S.V.; Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=972;
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